S1 Table. STROBE Checklist

	Item No	Recommendation	Section, Paragraph
Title and abstract	1	(*a*) Indicate the study's design with a commonly used term in the title or the abstract	Abstract, Paragraph 2
		(*b*) Provide in the abstract an informative and balanced summary of what was done and what was found	Abstract, Paragraph 2
Introduction			
Background/rationale	2	Explain the scientific background and rationale for the investigation being reported	Introduction, Paragraphs 2-4
Objectives	3	State specific objectives, including any prespecified hypotheses	Introduction, Paragraph 5
Methods			
Study design	4	Present key elements of study design early in the paper	Methods, Paragraph 2-3
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection	Methods, Paragraph 2-3
Participants	6	(*a*) *Cohort study*—Give the eligibility criteria, and the sources and methods of selection of participants. Describe methods of follow-up *Case-control study*—Give the eligibility criteria, and the sources and methods of case ascertainment and control selection. Give the rationale for the choice of cases and controls *Cross-sectional study*—Give the eligibility criteria, and the sources and methods of selection of participants	Methods, Paragraph 2
		(*b*) *Cohort study*—For matched studies, give matching criteria and number of exposed and unexposed *Case-control study*—For matched studies, give matching criteria and the number of controls per case	n/a
Variables	7	Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable	Methods, Paragraphs 3-5
Data sources/ measurement	8*	For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group	Methods, Paragraphs 3-5
Bias	9	Describe any efforts to address potential sources of bias	Methods, Paragraphs 9-10
Study size	10	Explain how the study size was arrived at	Methods, Paragraph 2
Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen and why	Methods, Paragraphs 4-5
Statistical methods	12	(*a*) Describe all statistical methods, including those used to control for confounding	Methods, Paragraphs 6-7
		(*b*) Describe any methods used to examine subgroups and interactions	Methods, Paragraph 10
		(*c*) Explain how missing data were addressed	Methods, Paragraph 8
		(*d*) *Cohort study*—If applicable, explain how loss to follow-up was addressed	n/a

		Case-control study—If applicable, explain how matching of cases and controls was addressed *Cross-sectional study*—If applicable, describe analytical methods taking account of sampling strategy	
		(*e*) Describe any sensitivity analyses	Methods, Paragraphs 8-9

Results

Participants	13*	(a) Report numbers of individuals at each stage of study—eg numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed	Methods, Paragraph 2 Results, Paragraph 1
		(b) Give reasons for non-participation at each stage	Methods, Paragraph 2
		(c) Consider use of a flow diagram	S1 Fig
Descriptive data	14*	(a) Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders	Table 1
		(b) Indicate number of participants with missing data for each variable of interest	S1 Fig
		(c) *Cohort study*—Summarise follow-up time (eg, average and total amount)	n/a
Outcome data	15*	*Cohort study*—Report numbers of outcome events or summary measures over time	n/a
		Case-control study—Report numbers in each exposure category, or summary measures of exposure	n/a
		Cross-sectional study—Report numbers of outcome events or summary measures	Results, Paragraph 1
Main results	16	(*a*) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg, 95% confidence interval). Make clear which confounders were adjusted for and why they were included	Results, Paragraph 3-4
		(*b*) Report category boundaries when continuous variables were categorized	S4 Table
		(*c*) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	Results, Paragraph 3
Other analyses	17	Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses	Results, Paragraphs 4-6

Discussion

Key results	18	Summarise key results with reference to study objectives	Discussion, Paragraphs 1, 5, 7
Limitations	19	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias	Discussion, Paragraph 8
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence	Discussion, Paragraphs 1-7
Generalisability	21	Discuss the generalisability (external validity) of the study results	Discussion, Paragraph 8

Other information

Funding	22	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based	Acknowledgments

S2 Table. Data Sources and Years for County-Level Factors

Variable	Data Source:
% 65 Years and Older	Census Population Estimates, 2018
% Rural	Census Population Estimates, 2010
% Hispanic	Census Population Estimates, 2018
% Non-Hispanic Black	Census Population Estimates, 2018
% Non-Hispanic White	Census Population Estimates, 2018
Median Household Income	Small Area Income and Poverty Estimates, 2018
% with Some College or Higher	American Community Survey, 5-year estimates, 2014-2018
% Homeownership	American Community Survey, 5-year estimates, 2014-2018
% with Poor or Fair Health	Behavioral Risk Factor Surveillance System, 2017
% with Obesity	United States Diabetes Surveillance System, 2016
% who Smoke	Behavioral Risk Factor Surveillance System, 2017
% with Diabetes	United States Diabetes Surveillance System, 2016

S3 Table. Comparison of OLS, Indirectly Age Standardized and Negative Binomial Models

Model	Number of Excess Deaths per 1 Directly Coded Covid-19 Death	% Excess Deaths Not Attributed to Covid-19
OLS Model[a,b]	1.20 [95% CI (1.16, 1.24)]	17% [95% CI (14%, 19%)]
OLS Model, Age-Standardized[a,b,c]	1.15 [95% CI (1.12, 1.19)]	13% [95% CI (11%, 16%)]
Negative Binomial Model[d,e]	1.28	22%

a. The OLS models were specified as $M(i) = \alpha + \beta_1 M^*(i) + \beta_2 C(i)$, where $M(i)$ = Death rate from all causes in county i in 2020, $M^*(i)$ = Death rate from all causes, county i in 2013-2018, and $C(i)$ = Covid-19 death rate in county i in 2020. Model weighted by the 2020 population. For the Negative Binomial model, $M(i)$ = deaths from all-causes in county i in 2020 rather than the death rate, with the 2020 population used as an offset.

b. Number of excess deaths per 1 directly coded Covid-19 death is equivalent to the regression coefficient for directly coded Covid-19 deaths.

c. Death rates were indirectly age-standardized.

d. To calculate the number of excess deaths per 1 directly coded Covid-19 deaths, we used marginal prediction to calculate the all-cause death rate in 2020 at values of directly coded Covid-19 mortality that were +/- 0.1 deaths per 1000 people from the weighted mean of directly coded Covid-19 mortality. The change in all-cause mortality between these values was divided by 0.2 deaths per 1000 people to yield the number of excess deaths per 1 directly coded Covid-19 death.

e. A Poisson model was tested prior to the Negative Binomial model but was rejected due to poor goodness of fit.

S4 Table. Boundaries for Sociodemographic and Health Characteristic Quartiles[a]

Characteristics	Lower 25% Quartile		Upper 25% Quartile	
	Lowest Value	Highest Value	Lowest Value	Highest Value
% 65 or Older	7.4%	13.6%	17.6%	57.6%
% Rural	0%	1.3%	24.3%	100%
% Hispanic	0.6%	5.7%	26.0%	96.4%
% Non-Hispanic Black	0.1%	3.6%	18.6%	85.4%
% Non-Hispanic White	2.7%	42.1%	77.9%	97.9%
Median Household Income	25,385	52,577	74,686	140,382
% with Some College or Higher	20.4%	60.3%	71.8%	90.3%
% Homeownership	19.6%	56.9%	71.0%	89.8%
% Living with Poor or Fair Health	8.1%	14.0%	18.9%	41.0%
% with Obesity	14.4%	24.9%	32.8%	51.0%
% who Smoke	5.9%	12.6%	17.6%	41.5%
% with Diabetes	2.9%	8.4%	11.5%	34.1%

a. Quartiles are weighted by the estimated 2020 population.

S1 Fig. Flowchart Detailing Sample Exclusions

```
┌─────────────────────────────┐
│  Counties in the NCHS Database │
│  with Covid-19 and All-Cause  │
│    Mortality Data for 2020    │
│                               │
│          (n=3,140)            │
└─────────────────────────────┘
              │
              │        ┌─────────────────────────────────┐
              ├───────▶│  Excluded Counties Missing All-Cause │
              │        │   Mortality Data for 2013-2018   │
              │        │              (n=2)               │
              │        └─────────────────────────────────┘
              │
              │        ┌─────────────────────────────────┐
              ├───────▶│    Limited to Counties with 10+  │
              │        │        Covid-19 Deaths           │
              │        │             (n=526)              │
              │        └─────────────────────────────────┘
              │
              │        ┌─────────────────────────────────┐
              ├───────▶│    Limited to Counties with 20+  │
              │        │        Covid-19 Deaths           │
              │        │             (n=516)              │
              │        └─────────────────────────────────┘
              │
              ▼
┌─────────────────────────────┐
│ Final County Analytic Sample[a] │
│                               │
│          (n=2,096)            │
└─────────────────────────────┘
```
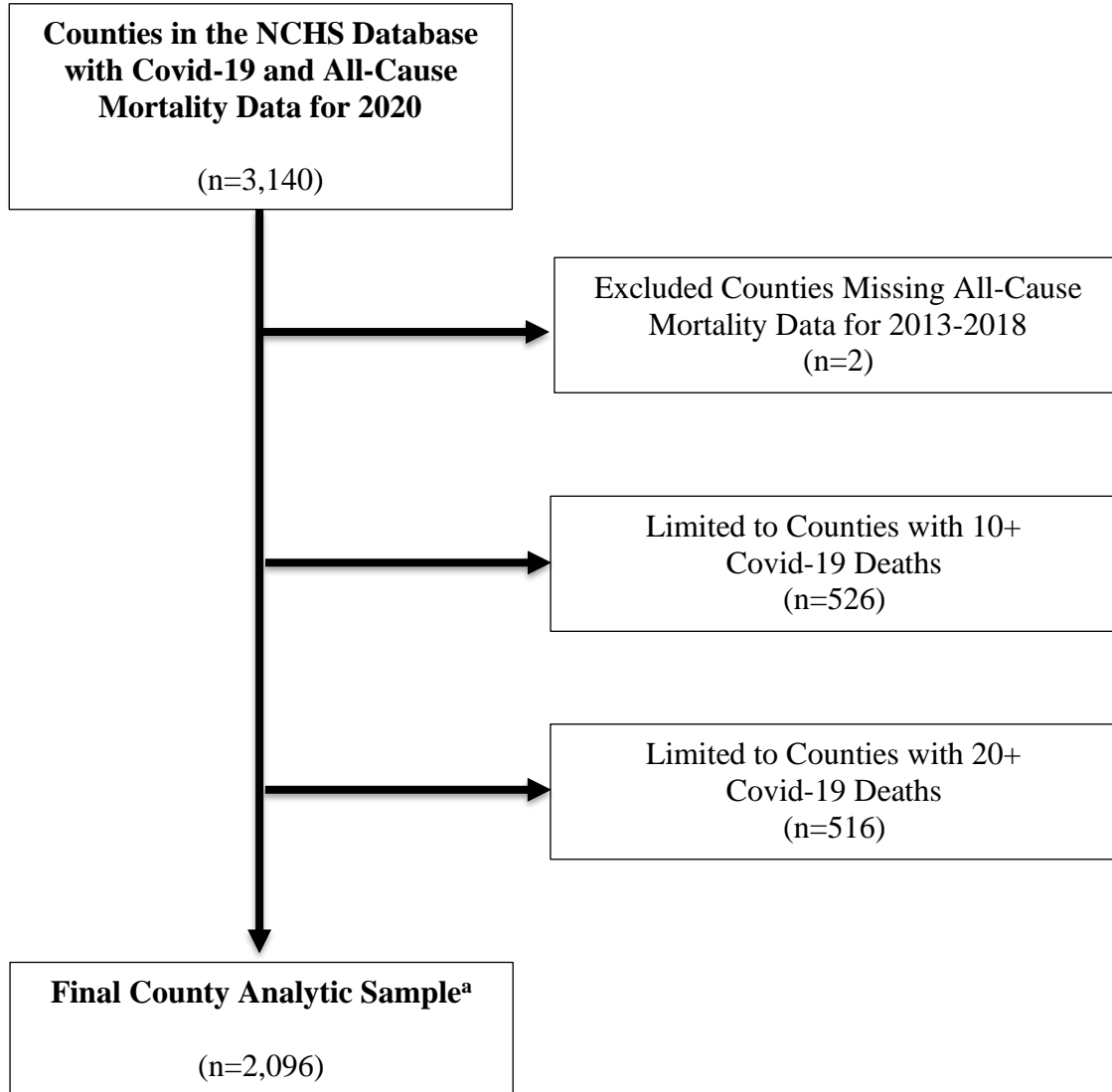
a. Counties had complete data for each of the sociodemographic and health characteristics we examined.

S2 Fig. US County Map Showing Geographic Distribution of Sample Counties (n=2,096)[a]
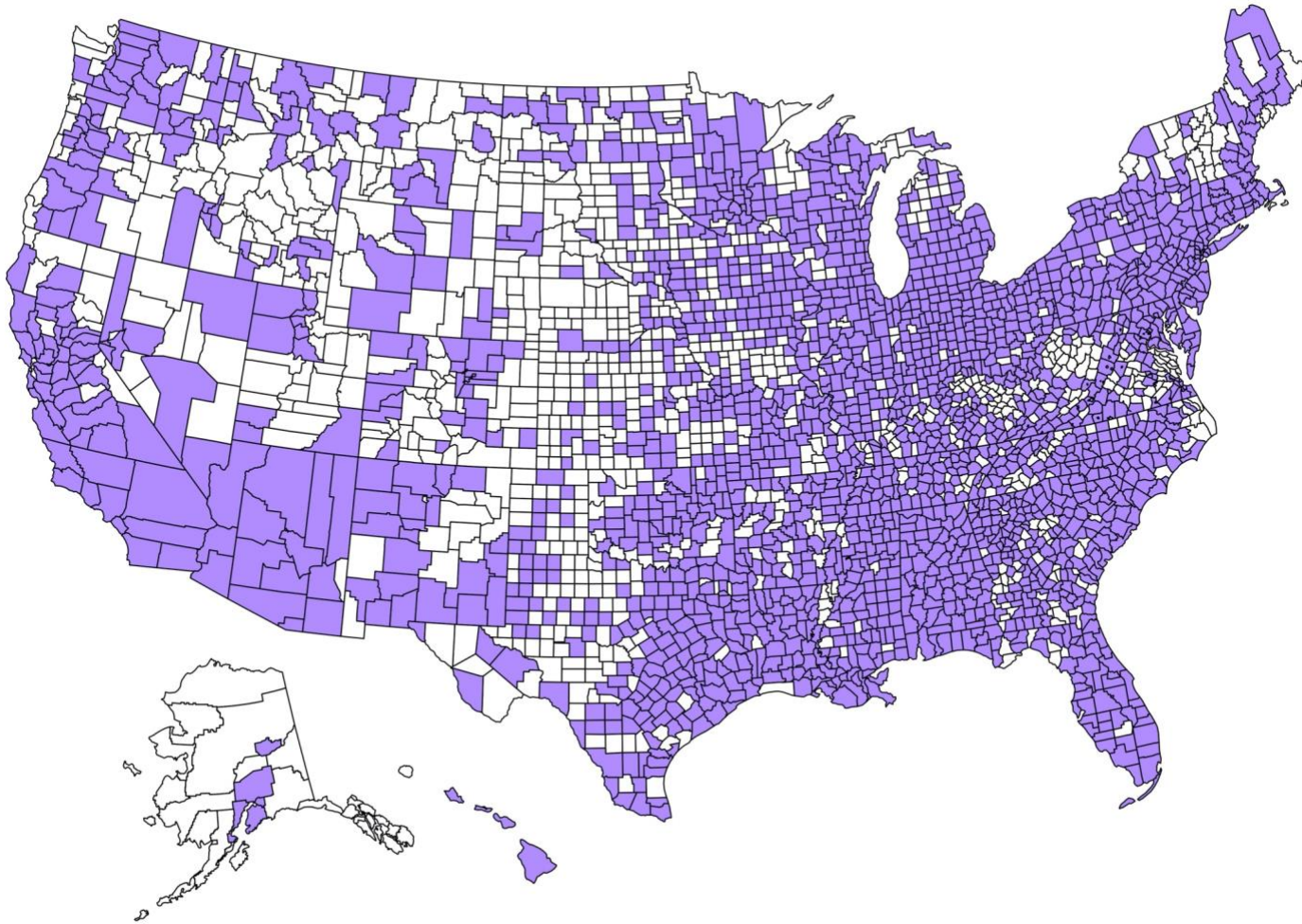
a. Map created using the usmap package in RStudio (https://CRAN.R-project.org/package=usmap)

S3 Fig. Relationship Between Indirectly Age Standardized All-Cause Mortality and Direct Covid-19 Mortality across Strata of Sociodemographic and Health Factors[a,b,c]

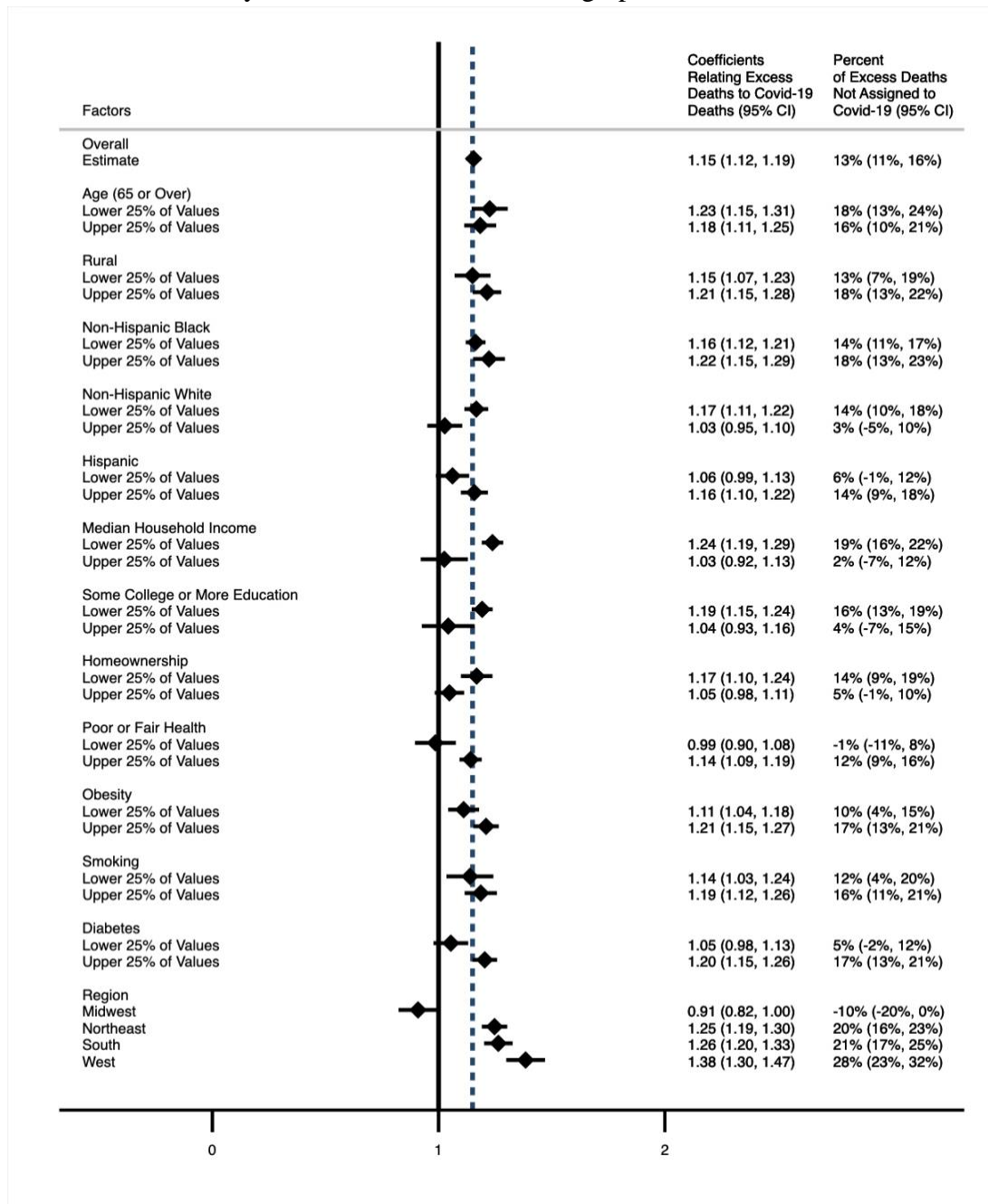| Factors	Coefficients Relating Excess Deaths to Covid-19 Deaths (95% CI)	Percent of Excess Deaths Not Assigned to Covid-19 (95% CI)
Overall Estimate	1.15 (1.12, 1.19)	13% (11%, 16%)
Age (65 or Over)		
Lower 25% of Values	1.23 (1.15, 1.31)	18% (13%, 24%)
Upper 25% of Values	1.18 (1.11, 1.25)	16% (10%, 21%)
Rural		
Lower 25% of Values	1.15 (1.07, 1.23)	13% (7%, 19%)
Upper 25% of Values	1.21 (1.15, 1.28)	18% (13%, 22%)
Non-Hispanic Black		
Lower 25% of Values	1.16 (1.12, 1.21)	14% (11%, 17%)
Upper 25% of Values	1.22 (1.15, 1.29)	18% (13%, 23%)
Non-Hispanic White		
Lower 25% of Values	1.17 (1.11, 1.22)	14% (10%, 18%)
Upper 25% of Values	1.03 (0.95, 1.10)	3% (-5%, 10%)
Hispanic		
Lower 25% of Values	1.06 (0.99, 1.13)	6% (-1%, 12%)
Upper 25% of Values	1.16 (1.10, 1.22)	14% (9%, 18%)
Median Household Income		
Lower 25% of Values	1.24 (1.19, 1.29)	19% (16%, 22%)
Upper 25% of Values	1.03 (0.92, 1.13)	2% (-7%, 12%)
Some College or More Education		
Lower 25% of Values	1.19 (1.15, 1.24)	16% (13%, 19%)
Upper 25% of Values	1.04 (0.93, 1.16)	4% (-7%, 15%)
Homeownership		
Lower 25% of Values	1.17 (1.10, 1.24)	14% (9%, 19%)
Upper 25% of Values	1.05 (0.98, 1.11)	5% (-1%, 10%)
Poor or Fair Health		
Lower 25% of Values	0.99 (0.90, 1.08)	-1% (-11%, 8%)
Upper 25% of Values	1.14 (1.09, 1.19)	12% (9%, 16%)
Obesity		
Lower 25% of Values	1.11 (1.04, 1.18)	10% (4%, 15%)
Upper 25% of Values	1.21 (1.15, 1.27)	17% (13%, 21%)
Smoking		
Lower 25% of Values	1.14 (1.03, 1.24)	12% (4%, 20%)
Upper 25% of Values	1.19 (1.12, 1.26)	16% (11%, 21%)
Diabetes		
Lower 25% of Values	1.05 (0.98, 1.13)	5% (-2%, 12%)
Upper 25% of Values	1.20 (1.15, 1.26)	17% (13%, 21%)
Region		
Midwest	0.91 (0.82, 1.00)	-10% (-20%, 0%)
Northeast	1.25 (1.19, 1.30)	20% (16%, 23%)
South	1.26 (1.20, 1.33)	21% (17%, 25%)
West	1.38 (1.30, 1.47)	28% (23%, 32%)

(x-axis: 0, 1, 2)

a. n = 2,096 counties

b. β_2 coefficients generated from primary model: $M(i) = \alpha + \beta_1 M^*(i) + \beta_2 C(i)$, where $M(i)$ = Death rate from all causes in county i in 2020, $M^*(i)$ = Death rate from all causes, county i in 2013-2018, and $C(i)$ = Covid-19 death rate in county i in 2020. The model was weighted by the 2020 population and fully stratified into population weighted quartiles for each sociodemographic or health factor. The coefficients for the upper and lower 25% of values for each factor are presented in this figure.

c. Sample interpretation: in counties with lower household income, for every 1 directly assigned Covid-19 death, there was an increase in 1.24 all-cause deaths, suggesting there were 0.24 deaths not assigned to Covid-19 for every 1 directly assigned Covid-19 death in these counties.

S4 Fig. Decomposition of 2020 Indirectly Age Standardized Excess Death Rates across Strata of Sociodemographic and Health Factors[a,b]
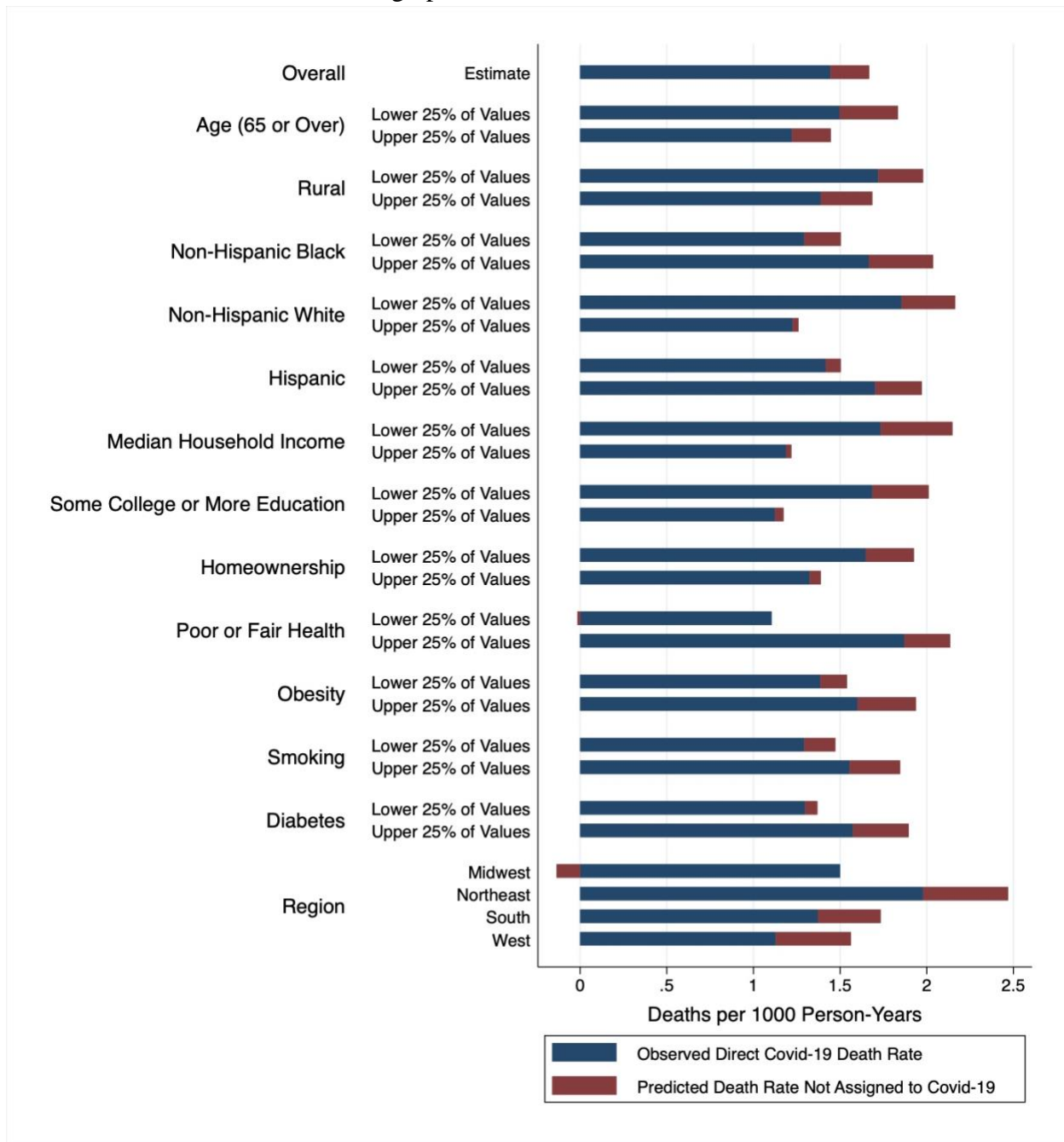
a. n = 2,096 counties

b. Predicted death rates generated from primary model: $M(i) = \alpha + \beta_1 M^*(i) + \beta_2 C(i)$, where $M(i) =$ Death rate from all causes in county i in 2020, $M^*(i) =$ Death rate from all causes, county i in 2013-2018, and $C(i) =$ Covid-19 death rate in county i in 2020. The model was weighted by the 2020 population and fully stratified into population weighted quartiles for each sociodemographic or health factor. The death rates for the upper and lower 25% of values for each factor are presented in this figure.